On page 8, delete the paragraph beginning on line 19, which reads:

[Also the prior art known in this field addressed only biotic stress (host-pathogen interaction), whereas our invention addresses a novel issue that is the area of abiotic stress (salinity stress).]

On page 9, the paragraph beginning on line 1 is rewritten to read:

A1 The polypeptide has glycosylation and phosphorylation sites. The said glycosylation is O glycosylation.

On page 9, delete the paragraph beginning on line 8, which reads:

[Said polypeptide has similarity with proteinase inhibitors of Bowman Birk type II of super family of proteinase inhibitors.]

On page 9, delete the paragraph beginning on line 16, which reads:

[The invention has use over a broad range of types of plants and organisms. Such plants *interalia* includes cotton, maize, rice, soybeans, sugar beet, wheat, fruit, vegetables and vines. The major use of proteinase inhibitors is against biotic stress response such as bacterial, fungal, pest resistance etc. in plants. It is also useful in the treatment of cancer, HIV and other areas in the animal systems. The gene may be useful for food processing and enzyme industries as an inhibitor of proteinase activity as a biological preservative.]

On page 11, the paragraph beginning on line 29 is rewritten to read:

A 2

The structure and function of AGT-SAL-11 was predicted using computational Biology, (Bioinformatics). Bioinformatics is a theoretical approach where predictions are carried out using computer applications; the Biological Data generated from the Laboratories till date is the source for the information on which the entire analysis was based.

On page 12, delete the paragraphs beginning on lines 21, 24, 26, 30, and 35, which read:

[AGT-SAL-11 molecule shows similarity with Proteinase Inhibitors of the Bowman – Birk II type of super-family of Proteinase Inhibitors, which are from the following species.]

[Ex. *Vicia faba, Vigna sp., Glycine max (Soyabean)* .]

[These molecules are generally bi-functional units, which can act on two different substrates. (Substrates being Chymotrypsin , Elastase, Trypsin, subtilisin) .]

[These Bowman –Birk type Proteinase inhibitors including AGT-SAL-11 molecules commonly have Glycosylation sites where a carbohydrate moiety can bind, most likely carbohydrates which bind with these molecules are Mannose sugars.]

[The 3D Structure of the Bowman–Birk type proteinase inhibitors shows the molecules tend to have an αβ type of folding.]

On page 12, the paragraph beginning on line 38 is rewritten to read:

A 3

The Secondary structure of AGTSAL-11 was predicted using the applications of Predict Protein Server. The results obtained are as

A3 Cont'd

On Page 13, the paragraph beginning on line 1 is rewritten to read:

a) The molecule shows a mixture of αβ type of secondary structure.

b) There are sites for Glycosylation and Phosphorylation (mostly Oglycosylation with Serine or Threonine residues).

On Page 13, delete the paragraph beginning on line 3, which reads:

Inhibitors of the Bowman Birk type are relatively small (about 70 amino acids length) and multiply cross linked with disulfide bridges. The Bowman- Birk inhibitors often display dual specificity, inhibiting both trypsin and chymotrypsin. No pattern has emerged to establish which inhibitors have protective effect and which do not. Inhibitor specificity does not appear to be the only factor, since some trypsin inhibitor are effective while others are not.

IN THE CLAIMS

Delete original claims 3, 4, 5 and 9.